SEQUENCE LISTING

(1)   GENERAL INFORMATION:

       (i)   APPLICANT: E. I. DU PONT DE NEMOURS AND
       COMPANY

       (ii)   TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
       INCREASING THE LYSINE AND
       THREONINE CONTENT OF THE SEEDS OF
       PLANTS

       (iii) NUMBER OF SEQUENCES: 107

       (iv)   CORRESPONDENCE ADDRESS:
       (A)   ADDRESSEE: E. I. DU PONT DE NEMOURS
       AND COMPANY
       (B)   STREET: 1007 MARKET STREET
       (C)   CITY: WILMINGTON
       (D)   STATE: DELAWARE
       (E)   COUNTRY: U.S.A.
       (F)   ZIP: 19898

       (v)   COMPUTER READABLE FORM:
       (A)   MEDIUM TYPE: FLOPPY DISK
       (B)   COMPUTER: IBM PC COMPATIBLE
       (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
       (D)   SOFTWARE: MICROSOFT WORD VERSION 2.0C

       (vi)   CURRENT APPLICATION DATA:
       (A)   APPLICATION NUMBER: US/10/023,066
       (B)   FILING DATE: 17-Dec-2001
       (C)   CLASSIFICATION:

       (viii)   ATTORNEY/AGENT INFORMATION:
       (A)   NAME: BARBARA C. SIEGELL
       (B)   REGISTRATION NUMBER: 30,684
       (C)   REFERENCE/DOCKET NUMBER: BB-1037-C

       (ix)   TELECOMMUNICATION INFORMATION:
       (A)   TELEPHONE: 302-992-4931
       (B)   TELEFAX: 302-773-0164
       (C)   TELEX: 835420

(2)   INFORMATION FOR SEQ ID NO:1:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 1350 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: DNA (genomic)

       (ix)   FEATURE:
       (A)   NAME/KEY: CDS
       (B)   LOCATION: 1..1350

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT      48
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
  1               5                  10                  15

TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC      96
Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
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                       20                         25                         30
GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG      144
Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
         35                      40                      45

GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC      192
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
         50                      55                      60

GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC      240
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
65                      70                      75                      80

CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT      288
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
                 85                      90                      95

GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT      336
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
                 100                     105                     110

GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG      384
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
         115                     120                     125

ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA      432
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
         130                     135                     140

GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC      480
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145                     150                     155                     160

GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA      528
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
                 165                     170                     175

GGC TTA GTG ATC ACC CAG GGA TTT ATC GGT AGC GAA AAT AAA GGT CGT      576
Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
                 180                     185                     190

ACA ACG ACG CTT GGC CGT GGA GGC AGC GAT TAT ACG GCA GCC TTG CTG      624
Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
                 195                     200                     205

GCG GAG GCT TTA CAC GCA TCT CGT GTT GAT ATC TGG ACC GAC GTC CCG      672
Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
210                     215                     220

GGC ATC TAC ACC ACC GAT CCA CGC GTA GTT TCC GCA GCA AAA CGC ATT      720
Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225                     230                     235                     240

GAT GAA ATC GCG TTT GCC GAA GCG GCA GAG ATG GCA ACT TTT GGT GCA      768
Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
                 245                     250                     255

AAA GTA CTG CAT CCG GCA ACG TTG CTA CCC GCA GTA CGC AGC GAT ATC      816
Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
                 260                     265                     270

CCG GTC TTT GTC GGC TCC AGC AAA GAC CCA CGC GCA GGT GGT ACG CTG      864
Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
                 275                     280                     285
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GTG TGC AAT AAA ACT GAA AAT CCG CCG CTG TTC CGC GCT CTG GCG CTT     912
Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
    290             295                 300

CGT CGC AAT CAG ACT CTG CTC ACT TTG CAC AGC CTG AAT ATG CTG CAT     960
Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
305             310                 315                 320

TCT CGC GGT TTC CTC GCG GAA GTT TTC GGC ATC CTC GCG CGG CAT AAT    1008
Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
            325                 330                 335

ATT TCG GTA GAC TTA ATC ACC ACG TCA GAA GTG AGC GTG GCA TTA ACC    1056
Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
            340                 345                 350

CTT GAT ACC ACC GGT TCA ACC TCC ACT GGC GAT ACG TTG CTG ACG CAA    1104
Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
            355                 360                 365

TCT CTG CTG ATG GAG CTT TCC GCA CTG TGT CGG GTG GAG GTG GAA GAA    1152
Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
370             375                 380

GGT CTG GCG CTG GTC GCG TTG ATT GGC AAT GAC CTG TCA AAA GCC TGC    1200
Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
385             390                 395                 400

GCC GTT GGC AAA GAG GTA TTC GGC GTA CTG GAA CCG TTC AAC ATT CGC    1248
Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
            405                 410                 415

ATG ATT TGT TAT GGC GCA TCC AGC CAT AAC CTG TGC TTC CTG GTG CCC    1296
Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
            420                 425                 430

GGC GAA GAT GCC GAG CAG GTG GTG CAA AAA CTG CAT AGT AAT TTG TTT    1344
Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
            435                 440                 445

GAG TAA                                                            1350
Glu *
    450
```

(2)   INFORMATION FOR SEQ ID NO:2:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG   36

(2)   INFORMATION FOR SEQ ID NO:3:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACCGCCAA ATTTGGAGAC AACAATTTCA GCCATG   36

(2)   INFORMATION FOR SEQ ID NO:4:

      (i)   SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 48 base pairs
      (B)   TYPE: nucleic acid
      (C)   STRANDEDNESS: single
      (D)   TOPOLOGY: linear

      (ii)   MOLECULE TYPE: DNA (genomic)

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT   48

(2)   INFORMATION FOR SEQ ID NO:5:

      (i)   SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 37 base pairs
      (B)   TYPE: nucleic acid
      (C)   STRANDEDNESS: single
      (D)   TOPOLOGY: linear

      (ii)   MOLECULE TYPE: DNA (genomic)

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTTC   37

(2)   INFORMATION FOR SEQ ID NO:6:

      (i)   SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 917 base pairs
      (B)   TYPE: nucleic acid
      (C)   STRANDEDNESS: single
      (D)   TOPOLOGY: linear

      (ii)   MOLECULE TYPE: DNA (genomic)

      (ix)   FEATURE:
      (A)   NAME/KEY: CDS
      (B)   LOCATION: 3..911

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:6:

CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC   47
   Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
   1   5   10   15

ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC   95
Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
              20   25   30

GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC   143
Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
          35   40   45

TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA   191
Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr
          50   55   60

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ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT  239
Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
        65                  70                  75

GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG  287
Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
    80                  85                  90                  95

ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC  335
Thr Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly
                100                 105                 110

CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG  383
Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu
                115                 120                 125

CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT  431
Leu Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys
            130                 135                 140

CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC  479
Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr
        145                 150                 155

ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC  527
Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala
160                 165                 170                 175

AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT  575
Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu
                180                 185                 190

GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG  623
Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu
                195                 200                 205

GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA  671
Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala
            210                 215                 220

TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG  719
Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala
        225                 230                 235

CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC  767
Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg
240                 245                 250                 255

TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC  815
Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
                260                 265                 270

AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA  863
Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu
                275                 280                 285

CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC
917
Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  *
        290                 295                 300
```

(2)   INFORMATION FOR SEQ ID NO:7:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 22 base pairs
        (B)   TYPE: nucleic acid

```
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

    (ii)   MOLECULE TYPE:  DNA (genomic)

    (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:7:

CTTCCCGTGA CCATGGGCCA TC                                        22

(2)    INFORMATION FOR SEQ ID NO:8:

        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  75 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

    (ii)   MOLECULE TYPE:  DNA (genomic)

    (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:8:

CATGGCTGGC TTCCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG CTAGCAACGG   60

TGGAAGAGTA CAATG                                                75

(2)    INFORMATION FOR SEQ ID NO:9:

        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  75 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

    (ii)   MOLECULE TYPE:  DNA (genomic)

    (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:9:

CATGCATTGT ACTCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT TGGTCTTCCT   60

CGTGGGGAAG CCAGC                                                75

(2)    INFORMATION FOR SEQ ID NO:10:

        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  90 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

    (ii)   MOLECULE TYPE:  DNA (genomic)

    (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:10:

CATGGCTTCC TCAATGATCT CCTCCCCAGC TGTTACCACC GTCAACCGTG CCGGTGCCGG   60

CATGGTTGCT CCATTCACCG GCCTCAAAAG                                90

(2)    INFORMATION FOR SEQ ID NO:11:

        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  90 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

    (ii)   MOLECULE TYPE:  DNA (genomic)
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGCTTTTG AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT   60

AACAGCTGGG GAGGAGATCA TTGAGGAAGC   90

(2)   INFORMATION FOR SEQ ID NO:12:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGGTTTGCT GTAATAGGTA CCA   23

(2)   INFORMATION FOR SEQ ID NO:13:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 31 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTGGTAC CTATTACAGC AAACCGGCAT G   31

(2)   INFORMATION FOR SEQ ID NO:14:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 27 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTCCTCAA TGATCTCCTC CCCAGCT   27

(2)   INFORMATION FOR SEQ ID NO:15:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 28 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATTGTACTC TTCCACCGTT GCTAGCAA   28

(2)   INFORMATION FOR SEQ ID NO:16:

       (i) SEQUENCE CHARACTERISTICS:

```
                (A)    LENGTH:   20 base pairs
                (B)    TYPE:  nucleic acid
                (C)    STRANDEDNESS:  single
                (D)    TOPOLOGY:  linear

                (ii)   MOLECULE TYPE:  DNA (genomic)

                (ix)   FEATURE:
                (A)    NAME/KEY:  misc_feature
                (B)    LOCATION:  1..20
                (D)    OTHER INFORMATION:  /product= "synthetic
         oligonucleotide"
         /standard_name= "SM
         70"

                (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:16:

         CTGACTCGCT GCGCTCGGTC                                    20

       (2)    INFORMATION FOR SEQ ID NO:17:

                 (i)   SEQUENCE CHARACTERISTICS:
                (A)    LENGTH:  24 base pairs
                (B)    TYPE:  nucleic acid
                (C)    STRANDEDNESS:  single
                (D)    TOPOLOGY:  linear

                (ii)   MOLECULE TYPE:  DNA (genomic)

                (ix)   FEATURE:
                (A)    NAME/KEY:  misc_feature
                (B)    LOCATION:  1..24
                (D)    OTHER INFORMATION:  /product= "synthetic
         oligonucleotide"
         /standard_name= "SM
         71"

                (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:17:

         TATTTTCTCC TTACGCATCT GTGC          .                    24

       (2)    INFORMATION FOR SEQ ID NO:18:

                 (i)   SEQUENCE CHARACTERISTICS:
                (A)    LENGTH:  27 base pairs
                (B)    TYPE:  nucleic acid
                (C)    STRANDEDNESS:  single
                (D)    TOPOLOGY:  linear

                (ii)   MOLECULE TYPE:  DNA (genomic)

                (ix)   FEATURE:
                (A)    NAME/KEY:   misc_feature
                (B)    LOCATION:  1..27
                (D)    OTHER INFORMATION:  /product= "synthetic
         oligonucleotide"
         /standard_name= "SM
         78"

                (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:18:

         TTCATCGATA GGCGACCACA CCCGTCC                            27

       (2)    INFORMATION FOR SEQ ID NO:19:

                 (i)   SEQUENCE CHARACTERISTICS:
```

```
        (A)   LENGTH:  27 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (ix)  FEATURE:
        (A)   NAME/KEY:  misc_feature
        (B)   LOCATION:  1..27
        (D)   OTHER INFORMATION:  /product= "synthetic
        oligonucleotide"
        /standard_name= "SM
        79"

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:19:

AATATCGATG CCACGATGCG TCCGGCG                              27

(2)   INFORMATION FOR SEQ ID NO:20:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  55 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (ix)  FEATURE:
        (A)   NAME/KEY:  misc_feature
        (B)   LOCATION:  1..55
        (D)   OTHER INFORMATION:  /product= "synthetic
        oligonucleotide"
        /standard_name= "SM
        81"

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:20:

CATGGAGGAG AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG      55

(2)   INFORMATION FOR SEQ ID NO:21:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  55 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (ix)  FEATURE:
        (A)   NAME/KEY:  misc_feature
        (B)   LOCATION:  1..55
        (D)   OTHER INFORMATION:  /product= "synthetic
        oligonucleotide"
        /standard_name= "SM
        80"

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:21:

AATTCGGTAC CTATCACGCC TTCATCTTCT CTTCCATCGC CTTCATCTTC TCCTC      55

(2)   INFORMATION FOR SEQ ID NO:22:

        (i)   SEQUENCE CHARACTERISTICS:
```

```
        (A)    LENGTH:   14 amino acids
        (B)    TYPE:   amino acid
        (C)    STRANDEDNESS:   unknown
        (D)    TOPOLOGY:   unknown

        (ii)   MOLECULE TYPE:   protein

        (ix)   FEATURE:
        (A)    NAME/KEY:  Protein
        (B)    LOCATION:   1..14
        (D)    OTHER INFORMATION:   /label= name
/note= "base gene
[(SSP5)2]"

        (xi)   SEQUENCE DESCRIPTION:   SEQ ID NO:22:

    Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
    1               5                   10
```

(2)   INFORMATION FOR SEQ ID NO:23:

```
        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:   21 base pairs
        (B)    TYPE:   nucleic acid
        (C)    STRANDEDNESS:   single
        (D)    TOPOLOGY:   linear

        (ii)   MOLECULE TYPE:   DNA (genomic)

        (ix)   FEATURE:
        (A)    NAME/KEY:  misc_feature
        (B)    LOCATION:   1..21
        (D)    OTHER INFORMATION:   /product=
"synthetic
oligonucleotide"
/standard_name= "SM
84"

        (xi)   SEQUENCE DESCRIPTION:   SEQ ID NO:23:
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GATGGAGGAG AAGATGAAGG C   21

(2)   INFORMATION FOR SEQ ID NO:24:

```
        (i)    SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:   21 base pairs
        (B)    TYPE:   nucleic acid
        (C)    STRANDEDNESS:   single
        (D)    TOPOLOGY:   linear

        (ii)   MOLECULE TYPE:   DNA (genomic)

        (ix)   FEATURE:
        (A)    NAME/KEY:  misc_feature
        (B)    LOCATION:   1..21
        (D)    OTHER INFORMATION:   /product= "synthetic
oligonucleotide"
/standard_name= "SM
85"

        (xi)   SEQUENCE DESCRIPTION:   SEQ ID NO:24:
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ATCGCCTTCA TCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:25:

```
      (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH:  21 base pairs
(B)   TYPE:  nucleic acid
(C)   STRANDEDNESS:  single
(D)   TOPOLOGY:  linear

(ii)  MOLECULE TYPE:  DNA (genomic)

(ix)  FEATURE:
(A)   NAME/KEY:  misc_feature
(B)   LOCATION:  1..21
(D)   OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
82"

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:25:
```

GATGGAGGAG AAGCTGAAGG C   21

(2)   INFORMATION FOR SEQ ID NO:26:

```
      (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH:  21 base pairs
(B)   TYPE:  nucleic acid
(C)   STRANDEDNESS:  single
(D)   TOPOLOGY:  linear

(ii)  MOLECULE TYPE:  DNA (genomic)

(ix)  FEATURE:
(A)   NAME/KEY:  misc_feature
(B)   LOCATION:  1..21
(D)   OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
83"

(xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:26:
```

ATCGCCTTCA GCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:27:

```
      (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH:  7 amino acids
(B)   TYPE:  amino acid
(C)   STRANDEDNESS:  unknown
(D)   TOPOLOGY:  unknown

(ii)  MOLECULE TYPE:  protein

(xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:27:
```

Met Glu Glu Lys Leu Lys Ala
1   5

(2)   INFORMATION FOR SEQ ID NO:28:

```
      (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH:  7 amino acids
(B)   TYPE:  amino acid
(C)   STRANDEDNESS:  unknown
(D)   TOPOLOGY:  unknown

(ii)  MOLECULE TYPE:  protein
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Glu Glu Lys Met Lys Ala
1   5

(2)   INFORMATION FOR SEQ ID NO:29:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 160 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

       (vii) IMMEDIATE SOURCE:
(B)   CLONE: C15

       (ix) FEATURE:
(A)   NAME/KEY: CDS
(B)   LOCATION: 2..151
(D)   OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.7.7.7.7.7.5"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1   5   10   15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
            20   25   30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
            35   40   45

AAG GCG TGATAGGTAC CG   160
Lys Ala
          50

(2)   INFORMATION FOR SEQ ID NO:30:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 49 amino acids
(B)   TYPE: amino acid
(D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1   5   10   15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35   40   45

Ala

(2)   INFORMATION FOR SEQ ID NO:31:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 160 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli
(G)   CELL TYPE: DH5 alpha

      (vii) IMMEDIATE SOURCE:
(B)   CLONE: C20

       (ix) FEATURE:
(A)   NAME/KEY: CDS
(B)   LOCATION: 2..151
(D)   OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.7.7.7.7.7.5"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
   1   5   10   15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
            20   25   30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG   142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
            35   40   45

AAG GCG TGATAGGTAC CG   160
Lys Ala
        50

(2)   INFORMATION FOR SEQ ID NO:32:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 49 amino acids
(B)   TYPE: amino acid
(D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1   5   10   15

```
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35                  40                  45

Ala
```

(2)   INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 139 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

    (vii) IMMEDIATE SOURCE:
(B)   CLONE: C30

    (ix) FEATURE:
(A)   NAME/KEY: CDS
(B)   LOCATION: 2..130
(D)   OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.7.7.7.7.5"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG        46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
   1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG    94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
            20                  25                  30

AAG CTG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CG          139
Lys Leu Lys Ala Met Glu Glu Lys Met Lys Ala
            35                  40
```

(2)   INFORMATION FOR SEQ ID NO:34:

    (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 42 amino acids
(B)   TYPE: amino acid
(D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: protein

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30
```

Leu Lys Ala Met Glu Glu Lys Met Lys Ala
      35   40

(2)   INFORMATION FOR SEQ ID NO:35:

       (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 97 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: double
       (D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (vi) ORIGINAL SOURCE:
       (B)   STRAIN: E. coli
       (G) CELL TYPE: DH5 alpha

       (vii) IMMEDIATE SOURCE:
       (B)   CLONE: D16

       (ix) FEATURE:
       (A)   NAME/KEY: CDS
       (B)   LOCATION: 2..88
       (D)   OTHER INFORMATION: /function= "synthetic
       storage protein"
       /product= "protein"
       /gene= "ssp"
       /standard_name=
       "5.5.5.5"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1   5   10   15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
            20   25

CG   97

(2)   INFORMATION FOR SEQ ID NO:36:

       (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 28 amino acids
       (B)   TYPE: amino acid
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: protein

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1   5   10   15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
            20   25

(2)   INFORMATION FOR SEQ ID NO:37:

       (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 118 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: double
       (D)   TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B)   CLONE: D20

(ix) FEATURE:
(A)   NAME/KEY: CDS
(B)   LOCATION: 2..109
(D)   OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1           5              10              15

GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG  94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu
            20              25              30

AAG ATG AAG GCG TGATAGGTAC CG                                     118
Lys Met Lys Ala
            35
```

(2)   INFORMATION FOR SEQ ID NO:38:

(i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 35 amino acids
(B)   TYPE: amino acid
(D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: protein

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1           5              10              15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys
            20              25              30

Met Lys Ala
        35
```

(2)   INFORMATION FOR SEQ ID NO:39:

(i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 97 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: DNA (genomic)

(vi)   ORIGINAL SOURCE:
(B)   STRAIN: E. coli

```
        (G)    CELL TYPE:  DH5 alpha

        (vii) IMMEDIATE SOURCE:
        (B)    CLONE:  D33

        (ix) FEATURE:
        (A)    NAME/KEY:  CDS
        (B)    LOCATION:  2..88
        (D)    OTHER INFORMATION:  /function= "synthetic
        storage protein"
        /product= "protein"
        /gene= "ssp"
        /standard_name=
        "5.5.5.5"

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:39:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG    46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1           5               10                  15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC    95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
             20                25

CG                                                               97

(2)    INFORMATION FOR SEQ ID NO:40:

        (i)  SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  28 amino acids
        (B)    TYPE:  amino acid
        (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  protein

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:40:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1           5               10                  15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
           20                25

(2)    INFORMATION FOR SEQ ID NO:41:

        (i)  SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  21 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  DNA (genomic)

        (ix) FEATURE:
        (A)    NAME/KEY:  misc_feature
        (B)    LOCATION:  1..21
        (D)    OTHER INFORMATION:  /product= "synthetic
        oligonucleotide"
        /standard_name= "SM
        86"

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:41:

GATGGAGGAG AAGCTGAAGA A                                      21
```

(2)   INFORMATION FOR SEQ ID NO:42:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..21
        (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
87"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCTTCTTCA GCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:43:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..21
        (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
88"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATGGAGGAG AAGCTGAAGT G   21

(2)   INFORMATION FOR SEQ ID NO:44:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..21
        (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
89"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCCACTTCA GCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:45:

          (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (ix) FEATURE:
          (A)   NAME/KEY: misc_feature
          (B)   LOCATION: 1..21
          (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
90"

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATGGAGGAG AAGATGAAGA A   21

(2)   INFORMATION FOR SEQ ID NO:46:

          (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (ix) FEATURE:
          (A)   NAME/KEY: misc_feature
          (B)   LOCATION: 1..21
          (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
91"

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTTCTTCA TCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:47:

          (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (ix) FEATURE:
          (A)   NAME/KEY: misc_feature
          (B)   LOCATION: 1..21
          (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
92"

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATGGAGGAG AAGATGAAGT G   21

(2)   INFORMATION FOR SEQ ID NO:48:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 21 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: DNA (genomic)

       (ix)   FEATURE:
       (A)   NAME/KEY: misc_feature
       (B)   LOCATION: 1..21
       (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
93"

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCCACTTCA TCTTCTCCTC C   21

(2)   INFORMATION FOR SEQ ID NO:49:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 7 amino acids
       (B)   TYPE: amino acid
       (C)   STRANDEDNESS: unknown
       (D)   TOPOLOGY: unknown

       (ii)   MOLECULE TYPE: protein

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Glu Glu Lys Leu Lys Lys
1   5

(2)   INFORMATION FOR SEQ ID NO:50:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 7 amino acids
       (B)   TYPE: amino acid
       (C)   STRANDEDNESS: unknown
       (D)   TOPOLOGY: unknown

       (ii)   MOLECULE TYPE: protein

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Glu Glu Lys Leu Lys Trp
1   5

(2)   INFORMATION FOR SEQ ID NO:51:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 7 amino acids
       (B)   TYPE: amino acid
       (C)   STRANDEDNESS: unknown
       (D)   TOPOLOGY: unknown

       (ii)   MOLECULE TYPE: protein

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Glu Lys Met Lys Lys
1   5

(2)   INFORMATION FOR SEQ ID NO:52:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 7 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: unknown
        (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: protein

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Glu Lys Met Lys Trp
1   5

(2)   INFORMATION FOR SEQ ID NO:53:

        (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 160 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: double
        (D)   TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (vi) ORIGINAL SOURCE:
        (B)   STRAIN: E. coli
        (G) CELL TYPE: DH5 alpha

        (vii) IMMEDIATE SOURCE:
        (B)   CLONE: 82-4

        (ix) FEATURE:
        (A)   NAME/KEY: CDS
        (B)   LOCATION: 2..151
        (D)   OTHER INFORMATION: /function= "synthetic
        storage protein
        /product= "protein"
        /gene= "ssp"
        /standard_name=
        "7.7.7.7.7.7.5"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG   46
  Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1   5   10   15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20   25   30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
                35   40   45

AAG GCG TGATAGGTAC CG   160
Lys Ala
        50

(2)   INFORMATION FOR SEQ ID NO:54:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 49 amino acids
        (B)   TYPE: amino acid

```
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  protein

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:54:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35                  40                  45

Ala


(2)    INFORMATION FOR SEQ ID NO:55:

        (i)  SEQUENCE CHARACTERISTICS:
    (A)    LENGTH:  97 base pairs
    (B)    TYPE:  nucleic acid
    (C)    STRANDEDNESS:  double
    (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  DNA (genomic)

        (vi) ORIGINAL SOURCE:
    (B)    STRAIN:  E. coli
    (G) CELL TYPE:  DH5 alpha

        (vii) IMMEDIATE SOURCE:
    (B)    CLONE:  84-H3

        (ix) FEATURE:
    (A)    NAME/KEY:  CDS
    (B)    LOCATION:  2..88
    (D)    OTHER INFORMATION:  /function= "synthetic
    storage protein
    /product= "protein"
    /gene= "ssp"
    /standard_name=
    "5.5.5.5"

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:55:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG    46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1               5                  10                  15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
            20                  25

CG                                                               97

(2)    INFORMATION FOR SEQ ID NO:56:

        (i)  SEQUENCE CHARACTERISTICS:
    (A)    LENGTH:  28 amino acids
    (B)    TYPE:  amino acid
    (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  protein
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1   5   10   15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
           20   25

(2)   INFORMATION FOR SEQ ID NO:57:

        (i) SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 97 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: double
        (D)   TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (vi) ORIGINAL SOURCE:
        (B)   STRAIN: E. coli
        (G)   CELL TYPE: DH5 alpha

        (vii) IMMEDIATE SOURCE:
        (B)   CLONE: 86-H23

        (ix) FEATURE:
        (A)   NAME/KEY: CDS
        (B)   LOCATION: 2..88
        (D)   OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.8.8.5"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met
   1   5   10   15

GAG GAG AAG CTG AAG AAG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
           20   25

CG   97

(2)   INFORMATION FOR SEQ ID NO:58:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 28 amino acids
        (B)   TYPE: amino acid
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: protein

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu
 1   5   10   15

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
           20   25

(2)   INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 112 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli
(G)   CELL TYPE: DH5 alpha

        (vii) IMMEDIATE SOURCE:
(B)   CLONE: 88-2

        (ix) FEATURE:
(A)   NAME/KEY: CDS
(B)   LOCATION: 2..103
(D)   OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
     "5.9.9.9.5"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG   46
  Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu
   1   5   10   15

AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94
Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met
                20   25   30

AAG GCG TGATAGGTAC CG   112
Lys Ala

(2)   INFORMATION FOR SEQ ID NO:60:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 33 amino acids
(B)   TYPE: amino acid
(D)   TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys
 1   5   10   15

Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys
                20   25   30

Ala

(2)   INFORMATION FOR SEQ ID NO:61:

        (i) SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 118 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

```
        (vi)  ORIGINAL SOURCE:
        (B)    STRAIN:  E. coli
        (G)    CELL TYPE:  DH5 alpha

        (vii) IMMEDIATE SOURCE:
        (B)    CLONE:  90-H8

        (ix) FEATURE:
        (A)    NAME/KEY:  CDS
        (B)    LOCATION:  2..109
        (D)    OTHER INFORMATION:  /function= "synthetic
        storage protein
        /product= "protein"
        /gene= "ssp"
        /standard_name=
        "5.10.10.10.5"

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:61:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG    46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met
  1               5               10                  15

GAG GAG AAG ATG AAG AAG ATG GAG GAG AAG ATG AAG AAG ATG GAA GAG 94
Glu Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu
              20              25                  30

AAG ATG AAG GCG TGATAGGTAC CG                                    118
Lys Met Lys Ala
          35

(2)   INFORMATION FOR SEQ ID NO:62:

        (i)  SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  35 amino acids
        (B)    TYPE:  amino acid
        (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  protein

        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:62:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu
 1               5               10                  15

Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu Lys
          20                  25                  30

Met Lys Ala
          35

(2)   INFORMATION FOR SEQ ID NO:63:

        (i)  SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  97 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  double
        (D)    TOPOLOGY:  linear

        (ii) MOLECULE TYPE:  DNA (genomic)

        (vi) ORIGINAL SOURCE:
        (B)    STRAIN:  E. coli
        (G)    CELL TYPE:  DH5 alpha
```

```
        (vii)  IMMEDIATE SOURCE:
        (B)    CLONE:  92-2

        (ix)  FEATURE:
        (A)    NAME/KEY:  CDS
        (B)    LOCATION:  2..88
        (D)    OTHER INFORMATION:  /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.11.11.5"

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:63:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG TGG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met
  1               5               10              15

GAG GAG AAG ATG AAG TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC     95
Glu Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
            20              25

CG                                                                 97

  (2)    INFORMATION FOR SEQ ID NO:64:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  28 amino acids
        (B)    TYPE:  amino acid
        (D)    TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  protein

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:64:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met Glu
 1               5               10              15

Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
          20              25

  (2)    INFORMATION FOR SEQ ID NO:65:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)    LENGTH:  84 base pairs
        (B)    TYPE:  nucleic acid
        (C)    STRANDEDNESS:  single
        (D)    TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (ix)  FEATURE:
        (A)    NAME/KEY:  misc_feature
        (B)    LOCATION:  1..84
        (D)    OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
96"

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:65:

GATGGAGGAA AAGATGAAGG CGATGGAGGA GAAAATGAAA GCTATGGAGG AAAAGATGAA 60

AGCGATGGAG GAGAAAATGA AGGC                                         84
```

(2)   INFORMATION FOR SEQ ID NO:66:

        (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 84 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: single
(D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: DNA (genomic)

(ix)   FEATURE:
(A)   NAME/KEY: misc_feature
(B)   LOCATION: 1..84
(D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
97"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATCGCCTTCA TTTTCTCCTC CATCGCTTTC ATCTTTTCCT CCATAGCTTT CATTTTCTCC 60

TCCATCGCCT TCATCTTTTC CTCC   84

(2)   INFORMATION FOR SEQ ID NO:67:

        (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 28 amino acids
(B)   TYPE: amino acid
(C)   STRANDEDNESS: unknown
(D)   TOPOLOGY: unknown

(ii)   MOLECULE TYPE: protein

(ix)   FEATURE:
(A)   NAME/KEY: Protein
(B)   LOCATION: 1..28
(D)   OTHER INFORMATION: /label= name
/note= "(SSP 5)4"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
1   5   10   15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
            20   25

(2)   INFORMATION FOR SEQ ID NO:68:

        (i)   SEQUENCE CHARACTERISTICS:
(A)   LENGTH: 84 base pairs
(B)   TYPE: nucleic acid
(C)   STRANDEDNESS: single
(D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: DNA (genomic)

(ix)   FEATURE:
(A)   NAME/KEY: misc_feature
(B)   LOCATION: 1..84
(D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATGGAGGAA AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 60

AGCGATGGAG GAGAAACTGA AGGC   84

(2)   INFORMATION FOR SEQ ID NO:69:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 84 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (ix) FEATURE:
       (A) NAME/KEY: misc_feature
       (B) LOCATION: 1..84
       (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
99"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATCGCCTTCA GTTTCTCCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 60

TCCATCGCTT TCAGCTTTTC CTCC   84

(2)   INFORMATION FOR SEQ ID NO:70:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 28 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: unknown
       (D) TOPOLOGY: unknown

       (ii) MOLECULE TYPE: protein

       (ix) FEATURE:
       (A) NAME/KEY: Protein
       (B) LOCATION: 1..28
       (D) OTHER INFORMATION: /label= name
/note= "(SSP 7)4"

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
1   5   10   15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala
            20   25

(2)   INFORMATION FOR SEQ ID NO:71:

       (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 84 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (ix) FEATURE:
       (A) NAME/KEY: misc_feature

```
(B)    LOCATION:  1..84
(D)    OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
100"
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATGGAGGAA AAGCTTAAGA AGATGGAAGA AAAGCTGAAA TGGATGGAGG AGAAACTCAA 60

AAAGATGGAG GAAAAGCTTA AATG   84

(2)   INFORMATION FOR SEQ ID NO:72:

```
(i)    SEQUENCE CHARACTERISTICS:
(A)    LENGTH:  84 base pairs
(B)    TYPE:  nucleic acid
(C)    STRANDEDNESS:  single
(D)    TOPOLOGY:  linear
```

(ii)   MOLECULE TYPE: DNA (genomic)

```
(ix)   FEATURE:
(A)    NAME/KEY:  misc_feature
(B)    LOCATION:  1..84
(D)    OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
101"
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATCCATTTAA GCTTTTCCTC CTACTTTTTG AGTTTCTCCT CCATCCATTT CAGCTTTTCT 60

TCCATCTTCT TAAGCTTTTC CTCC   84

(2)   INFORMATION FOR SEQ ID NO:73:

```
(i)    SEQUENCE CHARACTERISTICS:
(A)    LENGTH:  28 amino acids
(B)    TYPE:  amino acid
(C)    STRANDEDNESS:  unknown
(D)    TOPOLOGY:  unknown
```

(ii)   MOLECULE TYPE: protein

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu
1   5   10   15

Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp
            20   25

(2)   INFORMATION FOR SEQ ID NO:74:

```
(i) SEQUENCE CHARACTERISTICS:
(A)    LENGTH:  243 base pairs
(B)    TYPE:  nucleic acid
(C)    STRANDEDNESS:  double
(D)    TOPOLOGY:  linear
```

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B)   STRAIN: E. coli

```
      (G)   CELL TYPE:  DH5 alpha

      (vii) IMMEDIATE SOURCE:
      (B)   CLONE:  2-9

      (ix) FEATURE:
      (A)   NAME/KEY:  CDS
      (B)   LOCATION:  2..235
      (D)   OTHER INFORMATION:  /function= "synthetic
      storage protein
      /product= "protein"
      /gene= "ssp"
      /standard_name=
      "7.7.7.7.7.7.8.9.8.9.5"

         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:74:

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG
46
   Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1                 5                 10                15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG
94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
              20                25                30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG CTT
142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
          35                40                45

AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG
190
Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys
          50                55                60

ATG GAG GAA AAG CTT AAA TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC
242
Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala
      65                70                75

C
243

(2)   INFORMATION FOR SEQ ID NO:75:

      (i)   SEQUENCE CHARACTERISTICS:
      (A)   LENGTH:  77 amino acids
      (B)   TYPE:  amino acid
      (D)   TOPOLOGY:  linear

      (ii)  MOLECULE TYPE:  protein

      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:75:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1                 5                 10                15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
              20                25                30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
          35                40                45

Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys Met
```

Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala
 65   70   75

(2)   INFORMATION FOR SEQ ID NO:76:

        (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 175 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: double
       (D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

       (vi) ORIGINAL SOURCE:
       (B)   STRAIN: E. coli
       (G)   CELL TYPE: DH5 alpha

       (vii) IMMEDIATE SOURCE:
       (B)   CLONE: 5-1

       (ix) FEATURE:
       (A)   NAME/KEY: CDS
       (B)   LOCATION: 2..172
       (D)   OTHER INFORMATION: /function= "synthetic
       storage protein
       /product= "protein"
       /gene= "ssp"
       /standard_name=
       "5.5.5.7.7.7.7.5"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1   5   10   15

GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG   94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
           20   25   30

AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG   142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
           35   40   45

AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG   175
Lys Ala Met Glu Glu Lys Met Lys Ala
           50   55

(2)   INFORMATION FOR SEQ ID NO:77:

        (i) SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 56 amino acids
       (B)   TYPE: amino acid
       (D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1   5   10   15

Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
           20   25   30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
        35   40   45

Ala Met Glu Glu Lys Met Lys Ala
        50   55

(2)   INFORMATION FOR SEQ ID NO:78:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 187 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: double
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (vi)   ORIGINAL SOURCE:
        (B)   STRAIN: E. coli
        (G)   CELL TYPE: DH5 alpha

        (ix)   FEATURE:
        (A)   NAME/KEY: CDS
        (B)   LOCATION: 3..173
        (D)   OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"SSP-3-5"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:78:

CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG   47
   Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1   5   10   15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   95
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
            20   25   30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG ATG   143
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
            35   40   45

AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC   187
Lys Ala Met Glu Glu Lys Met Lys Ala
            50   55

(2)   INFORMATION FOR SEQ ID NO:79:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 56 amino acids
        (B)   TYPE: amino acid
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: protein

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
    1   5   10   15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20   25   30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35   40   45

Ala Met Glu Glu Lys Met Lys Ala
        50   55

(2)   INFORMATION FOR SEQ ID NO:80:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 61 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..61
        (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
107"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATGGAGGAG AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC 60

G   61

(2)   INFORMATION FOR SEQ ID NO:81:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 61 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..61
        (D)   OTHER INFORMATION: /product= "synthetic
ligonucleotide"
/standard_name= "SM
106"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCGGTAC CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT 60

C   61

(2)   INFORMATION FOR SEQ ID NO:82:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 16 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: unknown
        (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: protein

        (ix)   FEATURE:
        (A)   NAME/KEY: Protein

```
          (B)    LOCATION:  1..16
          (D)    OTHER INFORMATION:  /label= name
/note= "pSK34 base
gene"

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:82:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys
1               5                   10                  15


(2)     INFORMATION FOR SEQ ID NO:83:

          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  63 base pairs
          (B)    TYPE:  nucleic acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  DNA (genomic)

          (ix)   FEATURE:
          (A)    NAME/KEY:  misc_feature
          (B)    LOCATION:  1..63
          (D)    OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
110"

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:83:

GCTGGAAGAA AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA 60

GAA                                                              63

(2)     INFORMATION FOR SEQ ID NO:84:

          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  63 base pairs
          (B)    TYPE:  nucleic acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  DNA (genomic)

          (ix)   FEATURE:
          (A)    NAME/KEY:  misc_feature
          (B)    LOCATION:  1..63
          (D)    OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
111"

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:84:

AGCTTCTTCA TCTTTTCCTC AAGCCATTTC ATCTTGTCCT CCATAGCCTT CATCTTTTCT 60

TCC                                                              63

(2)     INFORMATION FOR SEQ ID NO:85:

          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  37 amino acids
          (B)    TYPE:  amino acid
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  protein
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
 1   5   10   15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
             20   25   30

Met Lys Val Met Lys
         35

(2)   INFORMATION FOR SEQ ID NO:86:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 37 amino acids
       (B)   TYPE: amino acid
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: protein

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
 1   5   10   15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
             20   25   30

Met Lys Val Met Lys
         35

(2)   INFORMATION FOR SEQ ID NO:87:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 62 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: DNA (genomic)

       (ix)   FEATURE:
       (A)   NAME/KEY: misc_feature
       (B)   LOCATION: 1..62
       (D)   OTHER INFORMATION: /product= "synthetic
       oligonucletide"
       /standard_name= "SM
       112"

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTCGAAGAA AGATGAAGGC AATGGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 60

AA   62

(2)   INFORMATION FOR SEQ ID NO:88:

       (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 62 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: DNA (genomic)

```
(ix)    FEATURE:
(A)     NAME/KEY:  misc_feature
(B)     LOCATION:  1..62
(D)     OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
113"

(xi)    SEQUENCE DESCRIPTION:   SEQ ID NO:88:
```

AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTGTCTT CCATTGCCTT CATCTTTCTT 60

CG   62

```
(2)     INFORMATION FOR SEQ ID NO:89:

        (i)     SEQUENCE CHARACTERISTICS:
        (A)     LENGTH:  37 amino acids
        (B)     TYPE:  amino acid
        (D)     TOPOLOGY:  linear

        (ii)    MOLECULE TYPE:  protein

        (xi)    SEQUENCE DESCRIPTION:   SEQ ID NO:89:
```

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys
 1   5   10   15

Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys
            20   25   30

Met Lys Val Met Lys
            35

```
(2)     INFORMATION FOR SEQ ID NO:90:

        (i)     SEQUENCE CHARACTERISTICS:
        (A)     LENGTH:  63 base pairs
        (B)     TYPE:  nucleic acid
        (C)     STRANDEDNESS:  single
        (D)     TOPOLOGY:  linear

        (ii)    MOLECULE TYPE:  DNA (genomic)

        (ix)    FEATURE:
        (A)     NAME/KEY:  misc_feature
        (B)     LOCATION:  1..63
        (D)     OTHER INFORMATION:  /product= "synthetic
oligonucleotide"
/standard_name= "SM
114"

        (xi)    SEQUENCE DESCRIPTION:   SEQ ID NO:90:
```

GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAACTGAAAG AGGAAATGAA 60

GAA   63

```
(2)     INFORMATION FOR SEQ ID NO:91:

        (i)     SEQUENCE CHARACTERISTICS:
        (A)     LENGTH:  63 base pairs
        (B)     TYPE:  nucleic acid
        (C)     STRANDEDNESS:  single
        (D)     TOPOLOGY:  linear
```

(ii)   MOLECULE TYPE: DNA (genomic)

        (ix)   FEATURE:
        (A)   NAME/KEY: misc_feature
        (B)   LOCATION: 1..63
        (D)   OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
115"

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTTCTTCA TTTCCTCTTT CAGTTTCCAC ATTTCGTCTT TCATCTTAGC CATTTCCTCC 60

TTG   63

(2)   INFORMATION FOR SEQ ID NO:92:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 107 amino acids
        (B)   TYPE: amino acid
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: protein

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys
 1   5   10   15

Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys
             20   25   30

Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys
         35   40   45

Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu
     50   55   60

Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu
 65   70   75   80

Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met
             85   90   95

Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys
            100   105

(2)   INFORMATION FOR SEQ ID NO:93:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 839 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGATCCCCCG GGCTGCAGGA ATTCTACGTA CCATATAGTA AGACTTTGTA TATAAGACGT 60

CACCTCTTAC GTGCATGGTT ATATGTGACA TGTGCAGTGA CGTTGTACCA TATAGTAAGA 120

CTTTGTATAT AAGACGTCAC CTCTTACGTG CATGGTTATA TGTGACATGT GCAGTGACGT 180

```
TAACCGCACC CTCCTTCCCG TCGTTTCCCA TCTCTTCCTC CTTTAGAGCT ACCACTATAT 240

AAATCAGGGC TCATTTTCTC GCTCCTCACA GGCTCATCAG CACCCCGGCA GTGCCACCCC 300

GACTCCCTGC ACCTGCCATG GGTACGCTAG CCCGGGAGAT CTGACAAAGC AGCATTAGTC 360

CGTTGATCGG TGGAAGACCA CTCGTCAGTG TTGAGTTGAA TGTTTGATCA ATAAAATACG 420

GCAATGCTGT AAGGGTTGTT TTTTATGCCA TTGATAATAC ACTGTACTGT TCAGTTGTTG 480

AACTCTATTT CTTAGCCATG CCAGTGCTTT TCTTATTTTG AATAACATTA CAGCAAAAAG 540

TTGAAAGACA AAAAAANNNN NCCCCGAACA GAGTGCTTTG GGTCCCAAGC TTCTTTAGAC 600

TGTGTTCGGC GTTCCCCCTA AATTTCTCCC CTATATCTCA CTCACTTGTC ACATCAGCGT 660

TCTCTTTCCC CTATATCTCC ACGCTCTACA GCAGTTCCAC CTATATCAAA CCTCTATACC 720

CCACCACAAC AATATTATAT ACTTTCATCT TCACCTAACT CATGTACCTT CCAATTTTTT 780

TCTACTAATA ATTATTTACG TGCACAGAAA CTTAGGCAAG GGAGAGAGAG AGCGGTACC  839
```

(2)   INFORMATION FOR SEQ ID NO:94:

    (i)   SEQUENCE CHARACTERISTICS:
  (A)   LENGTH: 43 base pairs
  (B)   TYPE: nucleic acid
  (C)   STRANDEDNESS: single
  (D)   TOPOLOGY: linear

   (ii)   MOLECULE TYPE: DNA (genomic)

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
CTAGAAGCCT CGGCAACGTC AGCAACGGCG GAAGAATCCG GTG            43
```

(2)   INFORMATION FOR SEQ ID NO:95:

    (i)   SEQUENCE CHARACTERISTICS:
  (A)   LENGTH: 43 base pairs
  (B)   TYPE: nucleic acid
  (C)   STRANDEDNESS: single
  (D)   TOPOLOGY: linear

   (ii)   MOLECULE TYPE: DNA (genomic)

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
CATGCACCGG ATTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT            43
```

(2)   INFORMATION FOR SEQ ID NO:96:

    (i)   SEQUENCE CHARACTERISTICS:
  (A)   LENGTH: 55 base pairs
  (B)   TYPE: nucleic acid
  (C)   STRANDEDNESS: single
  (D)   TOPOLOGY: linear

   (ii)   MOLECULE TYPE: DNA (genomic)

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
GATCCCATGG CGCCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCCGCCG CTCCT      55
```

(2)   INFORMATION FOR SEQ ID NO:97:

```
        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  55 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:97:

CTAGAGGAGC GGCGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG      55

   (2)   INFORMATION FOR SEQ ID NO:98:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  59 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:98:

CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC   59

   (2)   INFORMATION FOR SEQ ID NO:99:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  59 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:99:

TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC   59

   (2)   INFORMATION FOR SEQ ID NO:100:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  16 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:100:

GCGCCCACCG TGATGA                                                 16

   (2)   INFORMATION FOR SEQ ID NO:101:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH:  16 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS:  single
        (D)   TOPOLOGY:  linear

        (ii)  MOLECULE TYPE:  DNA (genomic)

        (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:101:
```

CACCGGATTC TTCCGC   16

(2)   INFORMATION FOR SEQ ID NO:102:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 372 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTAAGATTGG TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA
60

AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTTCCTAG
120

CTTCAGTTAG AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTCGGA GCAGACTCTG
180

AAGAGAAAAC AGATGTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT GCCAAAGAGA
240

CGGTTGAAGG TATTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC
300

TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG
360

CTTGTTGTAG CA
372

(2)   INFORMATION FOR SEQ ID NO:103:

        (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 323 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: DNA (genomic)

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGAAGCACAC TGCGACTCTT TTGGAATTCG GGGACATCAA GAATGGACAA ACAACAACCG
60

CTATGGCCAA GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA
120

AGATCAAGAC AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTTG CCAGCTTTGG
180

ATATATTGCA AGCATATGGT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG
240

TATATTGTTT CTNTCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA
300

GACCAGCAAA AAAAGGAGGA GGA
323

(2)   INFORMATION FOR SEQ ID NO:104:

```
          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  123 amino acids
          (B)    TYPE:  amino acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  protein

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:104:

Lys Ile Gly Lys Val Gln Gln Glu Asn Glu Ile Lys Glu Lys Pro Glu
1               5               10              15

Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Xaa
            20              25              30

Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln
        35              40              45

Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp
    50              55              60

Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr
65              70              75              80

Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp
            85              90              95

Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser
            100             105             110

Leu Leu Pro Ala Ser Cys His Ala Cys Cys Ser
        115             120
```

(2)   INFORMATION FOR SEQ ID NO:105:

```
          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  74 amino acids
          (B)    TYPE:  amino acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  protein

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:105:

Lys His Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln
1               5               10              15

Thr Thr Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly
            20              25              30

Ala Leu Leu Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg
        35              40              45

Pro Leu Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala
    50              55              60

Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu
65                  70
```

(2)   INFORMATION FOR SEQ ID NO:106:

```
          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  25 base pairs
```

```
          (B)    TYPE:  nucleic acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  DNA (genomic)

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:106:

ATTCCCCATG GTTTCGCCGA CGAAT
25


(2)     INFORMATION FOR SEQ ID NO:107:

          (i)    SEQUENCE CHARACTERISTICS:
          (A)    LENGTH:  29 base pairs
          (B)    TYPE:  nucleic acid
          (C)    STRANDEDNESS:  single
          (D)    TOPOLOGY:  linear

          (ii)   MOLECULE TYPE:  DNA (genomic)

          (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:107:

CTCTCGGTAC CTAGTACCTA CTGATCAAC
29
```